



PCT09

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,577A

DATE: 12/26/2002
TIME: 13:32:08

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

4 <110> APPLICANT: Dranoff, Glenn
5 Schmollinger, Jan
6 Hodi, F. Stephen
7 Mollick, Joseph
9 <120> TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
12 <130> FILE REFERENCE: 2486/109 (formerly 50059/005002)
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/762,577A
C--> 14 <141> CURRENT FILING DATE: 2002-08-29
14 <150> PRIOR APPLICATION NUMBER: 60/095,766
15 <151> PRIOR FILING DATE: 1998-08-07
17 <160> NUMBER OF SEQ ID NOS: 68
19 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

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495 <210> SEQ ID NO: 10
496 <211> LENGTH: 1168
497 <212> TYPE: PRT
498 <213> ORGANISM: Homo sapiens
500 <400> SEQUENCE: 10
501 Asn Ile Asp Leu Asp Leu Glu Ile Val Gln Ser Leu Gln His Gly His
502      1          5          10          15
503 Gly Gly Trp Thr Asp Gly Met Phe Glu Thr Leu Thr Thr Thr Gly Thr
504      20          25          30
505 Val Cys Gly Ile Asp Glu Asp His Asp Ile Val Val Gln Tyr Pro Ser
506      35          40          45
507 Gly Asn Arg Trp Thr Phe Asn Pro Ala Val Leu Thr Lys Ala Asn Ile
508      50          55          60
509 Val Arg Ser Gly Asp Ala Gln Gly Ala Glu Gly Gly Thr Ser Gln
510      65          70          75          80
511 Phe Gln Val Gly Asp Leu Val Gln Val Cys Tyr Asp Leu Glu Arg Ile
512      85          90          95
513 Lys Leu Leu Gln Arg Gly His Gly Glu Trp Ala Glu Ala Met Leu Pro
514      100          105          110
515 Thr Leu Gly Lys Val Gly Arg Val Gln Gln Ile Tyr Ser Asp Ser Asp
516      115          120          125
517 Leu Lys Val Glu Val Cys Gly Thr Ser Trp Thr Tyr Asn Pro Ala Ala
518      130          135          140
519 Val Ser Lys Val Ala Ser Ala Gly Ser Ala Ile Ser Asn Ala Ser Gly
520      145          150          155          160
521 Glu Arg Leu Ser Gln Leu Leu Lys Lys Leu Phe Glu Thr Gln Glu Ser
522      165          170          175

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621 Leu Phe Ser Arg Phe Lys Arg Asn Ile Val Glx Leu Glu Ser Asp Tyr
622 965 970 975
623 Gln Phe Gln Gly Asp Glx Glx Thr Arg Lys Gly Lys Ile Ser Asn Asn
624 980 985 990
625 Ser Gly Gln Leu Lys Arg Lys Lys Lys Arg Val Ser Ile Asn Trp Pro
626 995 1000 1005
627 Leu Thr Val Ala Phe Leu Thr Leu Ile Tyr Thr Leu Phe Cys Ser Ala
628 1010 1015 1020
629 Ser Val Phe Lys Lys Asn Leu Glx Lys Val Tyr Phe Arg Phe Ser Val
630 1025 1030 1035
631 Ile Thr Tyr Leu Gly Leu Ile Glx Pro Val Lys Glx His Cys Pro Ile
632 1045 1050 1055
633 Trp Thr Ser Glu Val Leu Phe Ser Phe Ala Asp Val His Ser Ile Pro
634 1060 1065 1070
635 Val Ile Cys Lys Ile Asn Ala Phe Ser Lys Lys Lys Ser Phe Leu Leu
636 1075 1080 1085
637 Cys Ile Ser Glx Phe Glx Gln Cys Glx Glx Phe Cys Leu His Tyr Arg
638 1090 1095 1100
639 Pro Tyr Phe His Tyr Leu Phe Leu Tyr Ser Ile Phe Cys Tyr Lys Glu
640 1105 1110 1115
641 Asn Ser Leu Ser Val Tyr Thr Tyr Gly Glx Gly Tyr Tyr Leu Asn Cys
642 1125 1130 1135
643 Gln Gln Tyr Pro Arg His Gly Gln Glx Pro Asn Tyr Lys Tyr Phe Arg
644 1140 1145 1150
645 Lys Ser Asp Gln Asp Met Tyr Arg Asn Val Cys Leu Pro Val Asp Phe
646 1155 1160 1165

move over to the left, one
space, and add the "0".

for explanation

As detected, see p. 11

1510 <210> SEQ ID NO: 40
1511 <211> LENGTH: 309
1512 <212> TYPE: DNA
1513 <213> ORGANISM: Homo sapiens
1515 <400> SEQUENCE: 40
E--> 1516 ncaaagtcaa atgaatttat tcagaaaagg ccttgcttgg tatcagacta agaaaagcag 60
E--> 1517 ccctgcccgc cgcccccan tccagaagg tcaatttaca aagacagggg cgcaggggag 120
1518 agctgggtgg ggaagacaca gccaggccag gagcttctgc aggccttggg ctccctgag 180
1519 ggcctgcgcg cttctgggtg gctgctatag tggccccaca ggaggccatg cactgtgggg 240
E--> 1520 gtcattgggt cacngggtca cgaangcata gcctnagggg gnagcccgtg agcagctccg 300
E--> 1521 ggagggcc
1533 <210> SEQ ID NO: 42
1534 <211> LENGTH: 166
1535 <212> TYPE: DNA
1536 <213> ORGANISM: Homo sapiens
1538 <400> SEQUENCE: 42
E--> 1539 cggcctgcag aagcntctcg gncntgggtg ttttttcccc acccagctct cccctgcgcc 60
E--> 1540 cttttttttt taaatnnacc cttctggagt gggggggcgc gggcagggct gcttttttna 120
E--> 1541 gtctgatgcc aagcaaggcc ttttttgaat aanttcattt ganttt 166
1543 <210> SEQ ID NO: 43
1544 <211> LENGTH: 209
1545 <212> TYPE: DNA
1546 <213> ORGANISM: Homo sapiens

same error

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1548 <400> SEQUENCE: 43
E--> 1549 gaaggtggat naggggtgctg tggacagtgc tacggtggcc agtgggtggtg cccagacctt      60
E--> 1550 ggcccttgcc gggteccctg ccccatcgcn cggccaaggc tggacacagt gagaacgggg      120
E--> 1551 ttgaggagga cacagaangt caaacggggc ccaaagaagg taccntggg gagcccatca      180
E--> 1552 gaganccan gccccagccn ggcagggac      209

1674 <210> SEQ ID NO: 46
1675 <211> LENGTH: 1299
1676 <212> TYPE: PRT
1677 <213> ORGANISM: Homo sapiens
1679 <400> SEQUENCE: 46
1680 Met Glu Pro Pro Ser Cys Ile Gln Asp Glu Pro Phe Pro His Pro Leu
1681 1 5 10 15
1682 Glu Pro Glu Pro Gly Val Ser Ala Gln Pro Gly Pro Gly Lys Pro Ser
1683 20 25 30
1684 Asp Lys Arg Phe Arg Leu Trp Tyr Val Gly Gly Ser Cys Leu Asp His
1685 35 40 45
1686 Arg Thr Thr Leu Pro Met Leu Pro Trp Leu Met Ala Glu Ile Arg Arg
1687 50 55 60
1688 Arg Ser Gln Lys Pro Glu Ala Gly Gly Cys Gly Ala Pro Ala Ala Arg
1689 65 70 75 80
1690 Glu Val Ile Leu Val Leu Ser Ala Pro Phe Leu Arg Cys Val Pro Ala
1691 85 90 95
1692 Pro Gly Ala Gly Ala Ser Gly Gly Thr Ser Pro Ser Ala Thr Gln Pro
1693 100 105 110
1694 Asn Pro Ala Val Phe Ile Phe Glu His Lys Ala Gln His Ile Ser Arg
1695 115 120 125
1696 Phe Ile His Asn Ser His Asp Leu Thr Tyr Phe Ala Tyr Leu Ile Lys
1697 130 135 140
1698 Ala Gln Pro Asp Asp Pro Glu Ser Gln Met Ala Cys His Val Phe Arg
1699 145 150 155 160
1700 Ala Thr Asp Pro Ser Gln Val Pro Asp Val Ile Ser Ser Ile Arg Gln
1701 165 170 175
1702 Leu Ser Lys Ala Ala Met Lys Glu Asp Ala Lys Pro Ser Lys Asp Asn
1703 180 185 190
1704 Glu Asp Ala Phe Tyr Asn Ser Gln Lys Phe Glu Val Leu Tyr Cys Gly
1705 195 200 205
1706 Lys Val Thr Val Thr His Lys Lys Ala Pro Ser Ser Leu Ile Asp Asp
1707 210 215 220
1708 Cys Met Glu Lys Phe Ser Leu His Glu Gln Gln Arg Leu Lys Ile Gln
1709 225 230 235 240
1710 Gly Glu Gln Arg Gly Pro Asp Pro Gly Glu Asp Leu Ala Asp Leu Glu
1711 245 250 255
1712 Val Val Val Pro Gly Ser Pro Gly Asp Cys Leu Pro Glu Glu Ala Asp
1713 260 265 270
1714 Gly Thr Asp Thr His Leu Gly Leu Pro Ala Gly Ala Ser Gln Pro Ala
1715 275 280 285
1716 Leu Thr Ser Ser Arg Val Cys Phe Pro Glu Arg Ile Leu Glu Asp Ser
1717 290 295 300
1718 Gly Phe Asp Glu Gln Gln Glu Phe Arg Ser Arg Cys Ser Ser Val Thr

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12/26/0

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1768 Ala Pro Ser Phe Thr Ala Pro Ser Phe Leu Lys Ser Phe Tyr Gln Asn
1769 705 710 715 720
1770 Ser Gly Arg Leu Ser Pro Gln Tyr Glu Asn Glu Ile Arg Gln Asp Thr
1771 725 730 735
1772 Ala Ser Glu Ser Ser Asp Gly Glu Gly Arg Lys Arg Thr Ser Ser Thr
1773 740 745 750
1774 Cys Ser Asn Glu Ser Leu Ser Val Gly Gly Thr Ser Val Thr Pro Arg
1775 755 760 765
1776 Arg Ile Ser Trp Arg Gln Arg Ile Phe Leu Arg Val Ala Ser Pro Met
1777 770 775 780
1778 Asn Lys Ser Pro Ser Ala Met Gln Gln Gln Asp Gly Leu Asp Arg Asn
1779 785 790 795 800
1780 Glu Leu Leu Pro Leu Ser Pro Leu Ser Pro Thr Met Glu Glu Glu Pro
1781 805 810 815
1782 Leu Val Ile Phe Leu Ser Gly Glu Asp Asp Pro Glu Lys Ile Glu Glu
1783 820 825 830
1784 Arg Lys Lys Ser Lys Glu Leu Arg Ser Leu Trp Arg Lys Ala Ile His
1785 835 840 845
1786 Gln Gln Ile Leu Leu Leu Arg Met Glu Lys Glu Asn Gln Lys Leu Glu
1787 850 855 860
1788 Gly Ala Ser Arg Asp Glu Leu Gln Ser Arg Lys Val Lys Leu Asp Tyr
1789 865 870 875 880
1790 Glu Glu Val Gly Ala Cys Gln Lys Glu Val Leu Ile Thr Trp Asp Lys
1791 885 890 895
1792 Lys Leu Leu Asn Cys Arg Ala Lys Ile Arg Cys Asp Met Glu Asp Ile
1793 900 905 910
1794 His Thr Leu Leu Lys Glu Gly Val Pro Lys Ser Arg Arg Gly Glu Ile
1795 915 920 925
1796 Trp Gln Phe Leu Ala Leu Gln Tyr Arg Leu Arg His Arg Leu Pro Asn
1797 930 935 940
1798 Lys Gln Gln Pro Pro Asp Ile Ser Tyr Lys Glu Leu Leu Lys Gln Leu
1799 945 950 955 960
1800 Thr Ala Gln Gln His Ala Ile Leu Val Asp Leu Gly Arg Thr Phe Pro
1801 965 970 975
1802 Thr His Pro Tyr Phe Ser Val Gln Leu Gly Pro Gly Gln Leu Ser Leu
1803 980 985 990
1804 Phe Asn Leu Leu Lys Ala Tyr Ser Leu Leu Asp Lys Glu Val Gly Tyr
1805 995 1000 1005
1806 Cys Gln Gly Ile Ser Phe Val Ala Gly Val Leu Leu His Met Ser
1807 1010 1015 1020
1808 Glu Glu Gln Ala Phe Glu Met Leu Lys Phe Leu Met Tyr Asp Leu Gly
E--> 1809 1025 1030 1035 1040
1810 Phe Arg Lys Gln Tyr Arg Pro Asp Met Met Ser Leu Gln Ile Gln Met
1811 1045 1050 1055
1812 Tyr Gln Leu Ser Arg Leu Leu His Asp Tyr His Arg Asp Leu Tyr Asn
1813 1060 1065 1070
1814 His Leu Glu Glu Asn Glu Ile Ser Pro Ser Leu Tyr Ala Ala Pro Trp
1815 1075 1080 1085
1816 Phe Leu Thr Leu Phe Ala Ser Gln Phe Ser Leu Gly Phe Val Ala Arg

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1817      1090      1095      1100
1818 Val Phe Asp Ile Ile Phe Leu Gln Gly Thr Glu Val Ile Phe Lys Val
E--> 1819 1105      1110      1115      1120
1820 Ala Leu Ser Leu Leu Ser Ser Gln Glu Thr Leu Ile Met Glu Cys Glu
1821      1125      1130      1135
1822 Ser Phe Glu Asn Ile Val Glu Phe Leu Lys Asn Thr Leu Pro Asp Met
1823      1140      1145      1150
1824 Asn Thr Ser Glu Met Glu Lys Ile Ile Thr Gln Val Phe Glu Met Asp
1825      1155      1160      1165
1826 Ile Ser Lys Gln Leu His Ala Tyr Glu Val Glu Tyr His Val Leu Gln
1827      1170      1175      1180
1828 Asp Glu Leu Gln Glu Ser Ser Tyr Ser Cys Glu Asp Ser Glu Thr Leu
E--> 1829 1185      1190      1195      1200
1830 Glu Lys Leu Glu Arg Ala Asn Ser Gln Leu Lys Arg Gln Asn Met Asp
1831      1205      1210      1215
1832 Leu Leu Glu Lys Leu Gln Val Ala His Thr Lys Ile Gln Ala Leu Glu
1833      1220      1225      1230
1834 Ser Asn Leu Glu Asn Leu Leu Thr Arg Glu Thr Lys Met Lys Ser Leu
1835      1235      1240      1245
1836 Ile Arg Thr Leu Glu Gln Glu Lys Met Ala Tyr Gln Lys Thr Val Glu
1837      1250      1255      1260
1838 Gln Leu Arg Lys Leu Leu Pro Ala Asp Ala Leu Ala Asn Cys Asp Leu
E--> 1839 1265      1270      1275      1280
1840 Leu Leu Arg Asp Leu Asn Cys Asn Pro Asn Asn Lys Ala Lys Ile Gly
1841      1285      1290      1295
1842 Asn Lys Pro
1969 <210> SEQ ID NO: 49
1970 <211> LENGTH: 226
1971 <212> TYPE: DNA
1972 <213> ORGANISM: Homo sapiens
1974 <400> SEQUENCE: 49
1975 ctgggatact cccctcccag ggtgtctggt ggcaggcctg tgcctatccc tgctgtcccc 60
1976 aggggtggcc ccgggggtca ggagctccag aagggccagc tgggcatatt ctgagattgg 120
E--> 1977 ccattcagccc ccattttctgc tgcaaacctg gtcagagcca gtnttccntc catgggacct 180
1978 aaagacagtg ccaagtgcct gcaccgtgga ccacagccga gccact 226
2262 <210> SEQ ID NO: 62
2263 <211> LENGTH: 607
2264 <212> TYPE: DNA
2265 <213> ORGANISM: Homo sapiens
2267 <400> SEQUENCE: 62
2268 ttttcagcat gagaatatgt gaatatgttt atttaggttt aacttacttc ttactatata 60
2269 gatttggctt gttttttata ataacaactg atatatgatt cacaaaaaag cagagaagag 120
2270 taagagaaaag agagagaaat ggagaaagag aagaaaaaag ggataaagaa tgaaagagag 180
2271 aaagagaata ccattctcta aaggaagagg tgcagaaaat tccattatcc tttcttcttg 240
2272 atcatgcctt gtatgattgg cagccaaact agccactgt gaaacccaac gtttgcttcc 300
2273 agatgaagat gtgccttcct ctgagtgggtg aaatccagat gtagtccagt gttttctttc 360
2274 ttccattact gctgcagcag aactgagagc ccaatctttt attagatcct tatgtttttc 420
2275 gttgataaca ggcctattat aatccgattg tcatctactc caaacacaac agctggctcg 480
2276 atgctttcag tagccggacc tctgtagctt ttgtgttcga atggtggcgt ctaagtgttc 540

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— No found see p11

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2277 ctcaagagtt gcacgtttgc tacagcgccg tgagccccag cgttctctga atcacttgcg 600
607

E--> 2278 tncatca

2280 <210> SEQ ID NO: 63

2281 <211> LENGTH: 402

2282 <212> TYPE: DNA

2283 <213> ORGANISM: Homo sapiens

2285 <400> SEQUENCE: 63

E--> 2286 ggcagagcac agaccaagcc aggagatgga taaagttaa aaaatcaagc aacttctgct 60
2287 acttctgaaa aggataatga tgatgaccaa agtgacaagg gtacttatac cattgagtta 120
2288 gagaatccca acagtgagga agtggaagca agaaaaatga ttcacaagggt aaataattga 180
2289 aatttgagtg tgatcttagt tgttgtgtgg tgtatttgac tgggtgaaat tattggagag 240
2290 tcagcatgag atgttgtcat gcagtcagtg gtatgtgaat tttagggttt tattagggaa 300
2291 ctgcaagact aacagtaaga ccaacatgct ttgtgatttt atttgctgat attctgaatt 360
2292 tacctgagtt tcatacataa agctctgtac atttaaaagg tt 402

2294 <210> SEQ ID NO: 64

2295 <211> LENGTH: 607

2296 <212> TYPE: DNA

2297 <213> ORGANISM: Homo sapiens

2299 <400> SEQUENCE: 64

2300 ttttcagcat gagaatatgt gaatatgttt atttagggttt aacttacttc ttactatata 60
2301 gatttggcctt gttttttata ataacaactg atatatgatt cacaaaaaag cagagaagag 120
2302 taagagaaaag agagagaaaat ggagaaaagag aagaaaaaag ggataaagaa tgaagagag 180
2303 aaagagaata ccattctcta aaggaagagg tgcagaaaat tccattatcc tttcttctg 240
2304 atcatgcctt gtatgattgg cagccaaact agcccactgt gaaacccaac gtttgcttcc 300
2305 agatgaagat gtgccttcct ctgagtggtg aaatccagat gtagtcaagtg gttttcttcc 360
2306 ttccattact gctgcagcag aactgagagc ccaatctttt attagatctt tatgttttcc 420
2307 gttgataaca ggcttattat aatccgattg tcacttactc caaacacaac agctggctcg 480
2308 atgcttttcag tagccggacc tctgtagctt ttgtgttcga atgggtggcgt ctaagtgttc 540
2309 ctcaagagtt gcacgtttgc tacagcgccg tgagccccag cgttctctga atcacttgcg 600
607

E--> 2310 tncatca

2312 <210> SEQ ID NO: 65

2313 <211> LENGTH: 317

2314 <212> TYPE: DNA

2315 <213> ORGANISM: Homo sapiens

2317 <400> SEQUENCE: 65

E--> 2318 tggggcggtgt gtggaanaac gttantgccc agcggantag nggccccgga gcnegaccgc 60
E--> 2319 agcggcanan cgacaacagc ggcgacgacg acgacgacga ggtgggggga ggacggcggtg 120
E--> 2320 cgagagactc acggggacgc acgnccccgc ctcccccgtc cggtcctctc ctccacggta 180
2321 aggggatgac gtagctttgc caaagactta gaagctaagc agaaaatgag cttaacatcc 240
2322 tgggttttgg tgagcagtgagg aggcactcgc cacaggctgc cacgagaaat gatttttgtt 300
2323 ggaaaaaatg actgtga 317

2473 <210> SEQ ID NO: 68

2474 <211> LENGTH: 2349

2475 <212> TYPE: PRT

2476 <213> ORGANISM: Homo sapiens

2478 <400> SEQUENCE: 68

2479 Met Ala Ala Val Leu Gln Gln Val Leu Glu Arg Thr Glu Leu Asn Lys 15
2480 1 5 10
2481 Leu Pro Lys Ser Val Gln Asn Lys Leu Glu Lys Phe Leu Ala Asp Gln

12/26/02

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2580      805      810      815
2581 Thr Asn Leu Gln Thr Ile Gln Gly Ile Leu Glu Arg Ser Glu Thr Glu
2582      820      825      830
2583 Thr Lys Gln Arg Leu Ser Ser Gln Ile Glu Lys Leu Glu His Glu Ile
2584      835      840      845
2585 Ser His Leu Lys Lys Lys Leu Glu Asn Glu Val Glu Gln Arg His Thr
2586      850      855      860
2587 Leu Thr Arg Asn Leu Asp Val Gln Leu Leu Asp Thr Lys Arg Gln Leu
2588 865      870      875      880
2589 Asp Thr Glu Thr Asn Leu His Leu Asn Thr Lys Glu Leu Leu Lys Asn
2590      885      890      895
2591 Ala Gln Lys Glu Ile Ala Thr Leu Lys Gln His Leu Ser Asn Met Glu
2592      900      905      910
2593 Val Gln Val Ala Ser Gln Ser Ser Gln Arg Thr Gly Lys Gly Gln Pro
2594      915      920      925
2595 Ser Asn Lys Glu Asp Val Asp Asp Leu Val Ser Gln Leu Arg Gln Thr
2596      930      935      940
2597 Glu Glu Gln Val Asn Asp Leu Lys Glu Arg Leu Lys Thr Ser Thr Ser
2598 945      950      955      960
2599 Asn Val Glu Gln Tyr Gln Ala Met Val Thr Ser Leu Glu Glu Ser Leu
2600      965      970      975
2601 Asn Lys Glu Lys Gln Val Thr Glu Glu Val Arg Lys Asn Ile Glu Val
2602      980      985      990
2603 Arg Leu Lys Glu Ser Ala Glu Phe Gln Thr Gln Leu Glu Lys Lys Leu
2604      995      1000      1005
2605 Met Glu Val Glu Lys Glu Lys Gln Glu Leu Gln Asp Lys Arg Arg
2606      1010      1015      1020
2607 Ala Ile Glu Ser Met Glu Gln Gln Leu Ser Glu Leu Lys Lys Thr Leu
2608 1025      1030      1035      1040
E--> 2609 Ser Ser Val Gln Asn Glu Val Gln Glu Ala Leu Gln Arg Ala Ser Thr
2610      1045      1050      1055
2611 Ala Leu Ser Asn Glu Gln Gln Ala Arg Arg Asp Cys Gln Glu Ala
2612      1060      1065      1070
2613 Lys Ile Ala Val Glu Ala Gln Asn Lys Tyr Glu Arg Glu Leu Met Leu
2614      1075      1080      1085
2615 His Ala Ala Asp Val Glu Ala Leu Gln Ala Ala Lys Glu Gln Val Ser
2616      1090      1095      1100
2617 Lys Met Ala Ser Val Arg Gln His Leu Glu Glu Thr Thr Gln Lys Ala
2618 1105      1110      1115      1120
E--> 2619 Glu Ser Gln Leu Leu Glu Cys Lys Ala Ser Trp Glu Glu Arg Glu Arg
2620      1125      1130      1135
2621 Met Leu Lys Asp Glu Val Ser Lys Cys Val Cys Arg Cys Glu Asp Leu
2622      1140      1145      1150
2623 Glu Lys Gln Asn Arg Leu Leu His Asp Gln Ile Glu Lys Leu Ser Asp
2624      1155      1160      1165
2625 Lys Val Val Ala Ser Val Lys Glu Gly Val Gln Gly Pro Leu Asn Val
2626      1170      1175      1180
2627 Ser Leu Ser Glu Glu Gly Lys Ser Gln Glu Gln Ile Leu Glu Ile Leu
2628 1185      1190      1195      1200
E-->

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2629 Arg Phe Ile Arg Arg Glu Lys Glu Ile Ala Glu Thr Arg Phe Glu Val
2630                               1205          1210          1215
2631 Ala Gln Val Glu Ser Leu Arg Tyr Arg Gln Arg Val Glu Leu Leu Glu
2632                               1220          1225          1230
2633 Arg Glu Leu Gln Glu Leu Glu Asp Ser Leu Asn Ala Glu Arg Glu Lys
2634                               1235          1240          1245
2635 Val Gln Val Thr Ala Lys Thr Met Ala Gln His Glu Glu Leu Met Lys
2636                               1250          1255          1260
2637 Lys Thr Glu Thr Met Asn Val Val Met Glu Thr Asn Lys Met Leu Arg
2638 1265                               1270          1275          1280
E--> 2638 1265                               1270          1275          1280
2639 Glu Glu Lys Glu Arg Leu Glu Gln Asp Leu Gln Gln Met Gln Ala Lys
2640                               1285          1290          1295
2641 Val Arg Lys Leu Glu Leu Asp Ile Leu Pro Leu Gln Glu Ala Asn Ala
2642                               1300          1305          1310
2643 Glu Leu Ser Glu Lys Ser Gly Met Leu Gln Ala Glu Lys Lys Leu Leu
2644                               1315          1320          1325
2645 Glu Glu Asp Val Lys Arg Trp Lys Ala Arg Asn Gln His Leu Val Ser
2646                               1330          1335          1340
2647 Gln Gln Lys Asp Pro Asp Thr Glu Glu Tyr Arg Lys Leu Leu Ser Glu
2648 1345                               1350          1355          1360
E--> 2648 1345                               1350          1355          1360
2649 Lys Glu Val His Thr Lys Arg Ile Gln Gln Leu Thr Glu Glu Ile Gly
2650                               1365          1370          1375
2651 Arg Leu Lys Ala Glu Ile Ala Arg Ser Asn Ala Ser Leu Thr Asn Asn
2652                               1380          1385          1390
2653 Gln Asn Leu Ile Gln Ser Leu Lys Glu Asp Leu Asn Lys Val Arg Thr
2654                               1395          1400          1405
2655 Glu Lys Glu Thr Ile Gln Lys Asp Leu Asp Ala Lys Ile Ile Asp Ile
2656                               1410          1415          1420
2657 Gln Glu Lys Val Lys Thr Ile Thr Gln Val Lys Lys Ile Gly Arg Arg
2658 1425                               1430          1435          1440
E--> 2658 1425                               1430          1435          1440
2659 Tyr Lys Thr Gln Tyr Glu Glu Leu Lys Ala Gln Gln Asp Lys Val Met
2660                               1445          1450          1455
2661 Glu Thr Ser Ala Gln Ser Ser Gly Asp His Gln Glu Gln His Val Ser
2662                               1460          1465          1470
2663 Val Gln Glu Met Gln Glu Leu Lys Glu Thr Leu Asn Gln Ala Glu Thr
2664                               1475          1480          1485
2665 Lys Ser Lys Ser Leu Glu Ser Gln Val Glu Asn Leu Gln Lys Thr Leu
2666                               1490          1495          1500
2667 Ser Glu Lys Glu Thr Glu Ala Arg Asn Leu Gln Glu Gln Thr Val Gln
2668 1505                               1510          1515          1520
E--> 2668 1505                               1510          1515          1520
2669 Leu Gln Ser Glu Leu Ser Arg Leu Arg Gln Asp Leu Gln Asp Arg Thr
2670                               1525          1530          1535
2671 Thr Gln Glu Glu Gln Leu Arg Gln Gln Ile Thr Glu Lys Glu Glu Lys
2672                               1540          1545          1550
2673 Thr Arg Lys Ala Ile Val Ala Ala Lys Ser Lys Ile Ala His Leu Ala
2674                               1555          1560          1565
2675 Gly Val Lys Asp Gln Leu Thr Lys Glu Asn Glu Glu Leu Lys Gln Arg
2676                               1570          1575          1580
2677 Asn Gly Ala Leu Asp Gln Gln Lys Asp Glu Leu Asp Val Arg Ile Thr

```

12/26/02

RAW SEQUENCE LISTING DATE: 12/26/2002
 PATENT APPLICATION: US/09/762,577A TIME: 13:32:08

Input Set : A:\pto.vsk.txt
 Output Set: N:\CRF4\12262002\I762577A.raw

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E--> 2678 1585                      1590                      1595                      1600
      2679 Ala Leu Lys Ser Gln Tyr Glu Gly Arg Ile Ser Arg Leu Glu Arg Glu
      2680                      1605                      1610                      1615
      2681 Leu Arg Glu His Gln Glu Arg His Leu Glu Gln Arg Asp Glu Pro Gln
      2682                      1620                      1625                      1630
      2683 Glu Pro Ser Asn Lys Val Pro Glu Gln Gln Arg Gln Ile Thr Leu Lys
      2684                      1635                      1640                      1645
      2685 Thr Thr Pro Ala Ser Gly Glu Arg Gly Ile Ala Ser Thr Ser Asp Pro
      2686                      1650                      1655                      1660
      2687 Pro Thr Ala Asn Ile Lys Pro Thr Pro Val Val Ser Thr Pro Ser Lys
E--> 2688 1665                      1670                      1675                      1680
      2689 Val Thr Ala Ala Ala Met Ala Gly Asn Lys Ser Thr Pro Arg Ala Ser
      2690                      1685                      1690                      1695
      2691 Ile Arg Pro Met Val Thr Pro Ala Thr Val Thr Asn Pro Thr Thr Thr
      2692                      1700                      1705                      1710
      2693 Pro Thr Ala Thr Val Met Pro Thr Thr Gln Val Glu Ser Gln Glu Ala
      2694                      1715                      1720                      1725
      2695 Met Gln Ser Glu Gly Pro Val Glu His Val Pro Val Phe Gly Ser Thr
      2696                      1730                      1735                      1740
      2697 Ser Gly Ser Val Arg Ser Thr Ser Pro Asn Val Gln Pro Ser Ile Ser
E--> 2698 1745                      1750                      1755                      1760
      2699 Gln Pro Ile Leu Thr Val Gln Gln Gln Thr Gln Ala Thr Ala Phe Val
      2700                      1765                      1770                      1775
      2701 Gln Pro Thr Gln Gln Ser His Pro Gln Ile Glu Pro Ala Asn Gln Glu
      2702                      1780                      1785                      1790
      2703 Leu Ser Ser Asn Ile Val Glu Val Val Gln Ser Ser Pro Val Glu Arg
      2704                      1795                      1800                      1805
      2705 Pro Ser Thr Ser Thr Ala Val Phe Gly Thr Val Ser Ala Thr Pro Ser
      2706                      1810                      1815                      1820
      2707 Ser Ser Leu Pro Lys Arg Thr Arg Glu Glu Glu Glu Asp Ser Thr Ile
E--> 2708 1825                      1830                      1835                      1840
      2709 Glu Ala Ser Asp Gln Val Ser Asp Asp Thr Val Glu Met Pro Leu Pro
      2710                      1845                      1850                      1855
      2711 Lys Lys Leu Lys Ser Val Thr Pro Val Gly Thr Glu Glu Glu Val Met
      2712                      1860                      1865                      1870
      2713 Ala Glu Glu Ser Thr Asp Gly Glu Val Glu Thr Gln Val Tyr Asn Gln
      2714                      1875                      1880                      1885
      2715 Asp Ser Gln Asp Ser Ile Gly Glu Gly Val Thr Gln Gly Asp Tyr Thr
      2716                      1890                      1895                      1900
      2717 Pro Met Glu Asp Ser Glu Glu Thr Ser Gln Ser Leu Gln Ile Asp Leu
E--> 2718 1905                      1910                      1915                      1920
      2719 Gly Pro Leu Gln Ser Asp Gln Gln Thr Thr Thr Ser Ser Gln Asp Gly
      2720                      1925                      1930                      1935
      2721 Gln Gly Lys Gly Asp Asp Val Ile Val Ile Asp Ser Asp Asp Glu Glu
      2722                      1940                      1945                      1950
      2723 Glu Asp Glu Glu Asp Asp Asp Asp Asp Glu Asp Asp Thr Gly Met Gly
      2724                      1955                      1960                      1965
      2725 Asp Glu Gly Glu Asp Ser Asn Glu Gly Thr Gly Ser Ala Asp Gly Asn
      2726                      1970                      1975                      1980

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RAW SEQUENCE LISTING

DATE: 12/26/2002

PATENT APPLICATION: US/09/762,577A

TIME: 13:32:08

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF4\12262002\I762577A.raw

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2727 Asp Gly Tyr Glu Ala Asp Asp Ala Glu Gly Gly Asp Gly Thr Asp Pro
E--> 2728 1985 1990 1995 <2000
2729 Gly Thr Glu Thr Glu Glu Ser Met Gly Gly Gly Glu Gly Asn His Arg
2730 2005 2010 2015
2731 Ala Ala Asp Ser Gln Asn Ser Gly Glu Gly Asn Thr Gly Ala Ala Glu
2732 2020 2025 2030
2733 Ser Ser Phe Ser Gln Glu Val Ser Arg Glu Gln Gln Pro Ser Ser Ala
2734 2035 2040 2045
2735 Ser Glu Arg Gln Ala Pro Arg Ala Pro Gln Ser Pro Arg Arg Pro Pro
2736 2050 2055 2060
2737 His Pro Leu Pro Pro Arg Leu Thr Ile His Ala Pro Pro Gln Glu Leu
E--> 2738 2065 2070 2075 <2080
2739 Gly Pro Pro Val Gln Arg Ile Gln Met Thr Arg Arg Gln Ser Val Gly
2740 2085 2090 2095
2741 Arg Gly Leu Gln Leu Thr Pro Gly Ile Gly Gly Met Gln Gln His Phe
2742 2100 2105 2110
2743 Phe Asp Asp Glu Asp Arg Thr Val Pro Ser Thr Pro Thr Leu Val Val
2744 2115 2120 2125
2745 Pro His Arg Thr Asp Gly Phe Ala Glu Ala Ile His Ser Pro Gln Val
2746 2130 2135 2140
2747 Ala Gly Val Pro Arg Phe Arg Phe Gly Pro Pro Glu Asp Met Pro Gln
E--> 2748 2145 2150 2155 <2160
2749 Thr Ser Ser Ser His Ser Asp Leu Gly Gln Leu Ala Ser Gln Gly Gly
2750 2165 2170 2175
2751 Leu Gly Met Tyr Glu Thr Pro Leu Phe Leu Ala His Glu Glu Glu Ser
2752 2180 2185 2190
2753 Gly Gly Arg Ser Val Pro Thr Thr Pro Leu Gln Val Ala Ala Pro Val
2754 2195 2200 2205
2755 Thr Val Phe Thr Glu Ser Thr Thr Ser Asp Ala Ser Glu His Ala Ser
2756 2210 2215 2220
2757 Gln Ser Val Pro Met Val Thr Thr Ser Thr Gly Thr Leu Ser Thr Thr
E--> 2758 2225 2230 2235 <2240
2759 Asn Glu Thr Ala Thr Gly Asp Asp Gly Asp Glu Val Phe Val Glu Ala
2760 2245 2250 2255
2761 Glu Ser Glu Gly Ile Ser Ser Glu Ala Gly Leu Glu Ile Asp Ser Gln
2762 2260 2265 2270
2763 Gln Glu Glu Glu Pro Val Gln Ala Ser Asp Glu Ser Asp Leu Pro Ser
2764 2275 2280 2285
2765 Thr Ser Gln Asp Pro Pro Ser Ser Ser Ser Val Asp Thr Ser Ser Ser
2766 2290 2295 2300
2767 Gln Pro Lys Pro Phe Arg Arg Val Arg Leu Gln Thr Thr Leu Arg Gln
E--> 2768 2305 2310 2315 <2320
2769 Gly Val Arg Gly Arg Gln Phe Asn Arg Gln Arg Gly Val Ser His Ala
2770 2325 2330 2335
2771 Met Gly Gly Arg Gly Gly Ile Asn Arg Gly Asn Ile Asn
2772 2340 2345
2777 02486/00109 215857.1
E--> 2780 1

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-delete

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/09/762,577A

DATE: 12/26/2002

TIME: 13:32:09

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF4\12262002\I762577A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:24; Xaa Pos. 2,4,7,16
Seq#:30; Xaa Pos. 9,14,15,20
Seq#:40; N Pos. 1,80,254,265,275,282,290,304
Seq#:42; N Pos. 15,22,24,76,77,119,153,163
Seq#:43; N Pos. 11,90,138,166,185,190,200
Seq#:49; N Pos. 163,168
Seq#:62; N Pos. 602
Seq#:63; N Pos. 35
Seq#:64; N Pos. 602
Seq#:65; N Pos. 17,25,37,41,53,68,70,144

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/762,577A

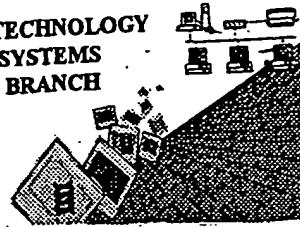
DATE: 12/26/2002

TIME: 13:32:09

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF4\12262002\I762577A.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:630 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:16
L:1516 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
M:340 Repeated in SeqNo=40
L:1539 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:42
M:340 Repeated in SeqNo=42
L:1549 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:43
M:340 Repeated in SeqNo=43
L:1809 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:1977 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:49
L:2278 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:62
L:2286 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
L:2310 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
L:2318 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:65
M:340 Repeated in SeqNo=65
L:2608 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:68
M:332 Repeated in SeqNo=68



05/11
PB

PH#8

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